



#5 OIPE

RAW SEQUENCE LISTING

DATE: 02/06/2002

PATENT APPLICATION: US/09/943,108A

TIME: 08:35:49

Input Set : N:\Crf3\RULE60\09943108.txt

Output Set: N:\CRF3\02062002\I943108A.raw

RECEIVED

NOV 14 2002

TECH CENTER 1600/290C

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4 <110> APPLICANT: Black, Michael T.
 7 <120> TITLE OF INVENTION: SIGNAL RECOGNITION PARTICLE POLYPEPTIDES
 8 AND POLYNUCLEOTIDES
 10 <130> FILE REFERENCE: GM50035
 12 <140> CURRENT APPLICATION NUMBER: 09/943,108A
 13 <141> CURRENT FILING DATE: 2001-08-30
 15 <150> PRIOR APPLICATION NUMBER: 09/035,382
 16 <151> PRIOR FILING DATE: 1998-05-03
 18 <160> NUMBER OF SEQ ID NOS: 8
 20 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1368
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Staphylococcus aureus
 27 <400> SEQUENCE: 1

ENTERED

28	atggcatttg	aaggcttatc	agaacgcctg	caagcgacga	tgcaaaaaaat	gcgtggtgaag	60
29	ggtaaaccta	ctgaagctga	tataaagata	atgatgcgtg	aagtaagatt	agcgttatatt	120
30	gaggctgacg	taaaccttaa	agtggtaaaa	gaatttatta	aaacagtatc	agaacgcgca	180
31	ttaggttccg	atgtaatgca	atcattaaca	ccagggaac	aagttattaa	aatagttcaa	240
32	gatgaattaa	cgaagttgat	gggtggagaa	aatacatcga	ttaatatgtc	aaataaacca	300
33	cctactgttg	ttatgatggt	tggtttacaa	ggtgctggta	aaacaacaac	tcgaggtaaa	360
34	ttagcattat	tgatgcgtaa	aaaatacaac	aaaaaaccta	tgtagttgc	agcagatatt	420
35	tatcgccag	cagcgataaa	tcaattacaa	acagtaggga	aacaaattga	tattcctgta	480
36	tacagtgaag	gagatcaagt	aaagccacaa	caaattgtaa	ctaattgcatt	aaaacatgct	540
37	aaagaagaac	atttagactt	tgtaatcatt	gatacagcag	gtcgattaca	catcgatgaa	600
38	gcattgatga	acgaattaaa	agaagtaaaa	gaaattgcta	aaccacacga	aattatgtta	660
39	gttgctcgatt	caatgacggg	tcaagatgct	gtcaatgttg	cagaatcttt	tgacgatcaa	720
40	cttgatgtca	caggtgttac	cttaactaaa	ttagatgggt	atacacgtgg	tggtgcagct	780
41	ttatctattc	gttcggtgac	acaaaaacca	attaaatttg	ttggtatgag	tgaaaagtta	840
42	gatggtttag	agctattcca	tcctgaacgt	atggcatcac	gtattttagg	tatgggtgat	900
43	gtgttaagtt	taattgaaaa	agcgcaacaa	gatgtggatc	aagaaaaagc	aaaagattta	960
44	gagaaaaaga	tgctgagtc	atcgtttact	ttagatgatt	ttttagaaca	acttgatcag	1020
45	gtgaaaaatc	taggaccact	ggatgatatt	atgaaaaatga	ttccaggtat	gaataaaatg	1080
46	aaagggctag	ataagcttaa	tatgagtga	aagcaaattg	atcatattaa	agcgattatc	1140
47	cagtcaatga	cgccggctga	aagaaacaat	ccagacacat	tgaatgtatc	acgtaaaaag	1200
48	cgtattgcta	aagggctctg	tcgttcatta	caagaagtca	atcgtttgat	gaaacaattt	1260
49	aacgatatga	agaaaatgat	gaaacaattc	actggtggcg	gtaaaaggtaa	aaaaggtaaa	1320
50	cgcaatcaaa	tgcaaaatat	gttaaaaggt	atgaatttac	cgtttttaa		1368

52 <210> SEQ ID NO: 2

53 <211> LENGTH: 455

54 <212> TYPE: PRT

55 <213> ORGANISM: Staphylococcus aureus

57 <400> SEQUENCE: 2

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58 Met Ala Phe Glu Gly Leu Ser Glu Arg Leu Gln Ala Thr Met Gln Lys
59 1 5 10 15
60 Met Arg Gly Lys Gly Lys Leu Thr Glu Ala Asp Ile Lys Ile Met Met
61 20 25 30
62 Arg Glu Val Arg Leu Ala Leu Phe Glu Ala Asp Val Asn Phe Lys Val
63 35 40 45
64 Val Lys Glu Phe Ile Lys Thr Val Ser Glu Arg Ala Leu Gly Ser Asp
65 50 55 60
66 Val Met Gln Ser Leu Thr Pro Gly Gln Gln Val Ile Lys Ile Val Gln
67 65 70 75 80
68 Asp Glu Leu Thr Lys Leu Met Gly Gly Glu Asn Thr Ser Ile Asn Met
69 85 90 95
70 Ser Asn Lys Pro Pro Thr Val Val Met Met Val Gly Leu Gln Gly Ala
71 100 105 110
72 Gly Lys Thr Thr Thr Ala Gly Lys Leu Ala Leu Leu Met Arg Lys Lys
73 115 120 125
74 Tyr Asn Lys Lys Pro Met Leu Val Ala Ala Asp Ile Tyr Arg Pro Ala
75 130 135 140
76 Ala Ile Asn Gln Leu Gln Thr Val Gly Lys Gln Ile Asp Ile Pro Val
77 145 150 155 160
78 Tyr Ser Glu Gly Asp Gln Val Lys Pro Gln Gln Ile Val Thr Asn Ala
79 165 170 175
80 Leu Lys His Ala Lys Glu Glu His Leu Asp Phe Val Ile Ile Asp Thr
81 180 185 190
82 Ala Gly Arg Leu His Ile Asp Glu Ala Leu Met Asn Glu Leu Lys Glu
83 195 200 205
84 Val Lys Glu Ile Ala Lys Pro Asn Glu Ile Met Leu Val Val Asp Ser
85 210 215 220
86 Met Thr Gly Gln Asp Ala Val Asn Val Ala Glu Ser Phe Asp Asp Gln
87 225 230 235 240
88 Leu Asp Val Thr Gly Val Thr Leu Thr Lys Leu Asp Gly Asp Thr Arg
89 245 250 255
90 Gly Gly Ala Ala Leu Ser Ile Arg Ser Val Thr Gln Lys Pro Ile Lys
91 260 265 270
92 Phe Val Gly Met Ser Glu Lys Leu Asp Gly Leu Glu Leu Phe His Pro
93 275 280 285
94 Glu Arg Met Ala Ser Arg Ile Leu Gly Met Gly Asp Val Leu Ser Leu
95 290 295 300
96 Ile Glu Lys Ala Gln Gln Asp Val Asp Gln Glu Lys Ala Lys Asp Leu
97 305 310 315 320
98 Glu Lys Lys Met Arg Glu Ser Ser Phe Thr Leu Asp Asp Phe Leu Glu
99 325 330 335
100 Gln Leu Asp Gln Val Lys Asn Leu Gly Pro Leu Asp Asp Ile Met Lys
101 340 345 350
102 Met Ile Pro Gly Met Asn Lys Met Lys Gly Leu Asp Lys Leu Asn Met
103 355 360 365
104 Ser Glu Lys Gln Ile Asp His Ile Lys Ala Ile Ile Gln Ser Met Thr
105 370 375 380
106 Pro Ala Glu Arg Asn Asn Pro Asp Thr Leu Asn Val Ser Arg Lys Lys

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107 385          390          395          400
108 Arg Ile Ala Lys Gly Ser Gly Arg Ser Leu Gln Glu Val Asn Arg Leu
109          405          410          415
110 Met Lys Gln Phe Asn Asp Met Lys Lys Met Met Lys Gln Phe Thr Gly
111          420          425          430
112 Gly Gly Lys Gly Lys Lys Gly Lys Arg Asn Gln Met Gln Asn Met Leu
113          435          440          445
114 Lys Gly Met Asn Leu Pro Phe
115          450          455
117 <210> SEQ ID NO: 3
118 <211> LENGTH: 792
119 <212> TYPE: DNA
120 <213> ORGANISM: Staphylococcus aureus
122 <400> SEQUENCE: 3
123 atggcatttg aaggcttatc agaacgcctg caagcgacga tgcaaaaaat gcgtggtaag      60
124 ggtaaaactta ctgaagctga tataaagata atgatgcgtg aagtaagatt agcgttattt      120
125 gaggctgacg taaactttaa agtggtaaaa gaatttatta aaacagtatc agaacgcgca      180
126 ttaggttccg atgtaatgca atcattaaca ccagggcaac aagttattaa aatagttcaa      240
127 gatgaattaa cgaagttagt ggggtggagaa aatacatcga ttaatatgtc aaataaacca      300
128 cctactgttg ttatgatggg tggtttaciaa ggtgctggta aaacaacaac tgcaggtaaa      360
129 ttagcattat tgatgcgtaa aaaatacaac aaaaaaccta tgttagtgtc agcagatatt      420
130 tatcgtccag cagcgataaa tcaattacaa acagtaggga aacaaattga tattcctgta      480
131 tacagtgaag gagatcaagt aaagccacaa caaattgtaa ctaatgcatt aaaacatgct      540
132 aaagaagaac attttagactt tgtaatcatt gatacagcag gtcgattaca catcgatgaa      600
133 gcattgatga acgaattaaa agaagtaaaa gaaattgcta aaccaaacga aattatgtta      660
134 gttgtcgatt caatgacggg tcaagatgct gtcaatgttg cagaatcttt tgacgatcaa      720
135 cttgatgtca caggtgttac cttaactaaa ttagatgggt ataccctggg tgggtgcagct      780
136 ttatctattc gt                                     792
138 <210> SEQ ID NO: 4
139 <211> LENGTH: 264
140 <212> TYPE: PRT
141 <213> ORGANISM: Staphylococcus aureus
143 <400> SEQUENCE: 4
144 Met Ala Phe Glu Gly Leu Ser Glu Arg Leu Gln Ala Thr Met Gln Lys
145 1          5          10          15
146 Met Arg Gly Lys Gly Lys Leu Thr Glu Ala Asp Ile Lys Ile Met Met
147          20          25          30
148 Arg Glu Val Arg Leu Ala Leu Phe Glu Ala Asp Val Asn Phe Lys Val
149          35          40          45
150 Val Lys Glu Phe Ile Lys Thr Val Ser Glu Arg Ala Leu Gly Ser Asp
151          50          55          60
152 Val Met Gln Ser Leu Thr Pro Gly Gln Gln Val Ile Lys Ile Val Gln
153          65          70          75          80
154 Asp Glu Leu Thr Lys Leu Met Gly Gly Glu Asn Thr Ser Ile Asn Met
155          85          90          95
156 Ser Asn Lys Pro Pro Thr Val Val Met Met Val Gly Leu Gln Gly Ala
157          100         105         110
158 Gly Lys Thr Thr Thr Ala Gly Lys Leu Ala Leu Leu Met Arg Lys Lys
159          115         120         125

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160 Tyr Asn Lys Lys Pro Met Leu Val Ala Ala Asp Ile Tyr Arg Pro Ala
161      130      135      140
162 Ala Ile Asn Gln Leu Gln Thr Val Gly Lys Gln Ile Asp Ile Pro Val
163 145      150      155      160
164 Tyr Ser Glu Gly Asp Gln Val Lys Pro Gln Gln Ile Val Thr Asn Ala
165      165      170      175
166 Leu Lys His Ala Lys Glu Glu His Leu Asp Phe Val Ile Ile Asp Thr
167      180      185      190
168 Ala Gly Arg Leu His Ile Asp Glu Ala Leu Met Asn Glu Leu Lys Glu
169      195      200      205
170 Val Lys Glu Ile Ala Lys Pro Asn Glu Ile Met Leu Val Val Asp Ser
171      210      215      220
172 Met Thr Gly Gln Asp Ala Val Asn Val Ala Glu Ser Phe Asp Asp Gln
173 225      230      235      240
174 Leu Asp Val Thr Gly Val Thr Leu Thr Lys Leu Asp Gly Asp Thr Arg
175      245      250      255
176 Gly Gly Ala Ala Leu Ser Ile Arg
177      260
179 <210> SEQ ID NO: 5
180 <211> LENGTH: 500
181 <212> TYPE: DNA
182 <213> ORGANISM: Staphylococcus aureus
184 <400> SEQUENCE: 5
185 aaacatcttg caaatgaatt taaatttaac gacttctcaa gacgtcgtat aaagtaaaca      60
186 atgatataaa tgatttatac ttgcaattaa ctattaaaa atagtaatat atatcttgcc      120
187 gtgctagggtg gggaggtagc ggttccctgt actcgaaatc cgctttatgc gaggcttaat      180
188 tcctttgttg aggccgtatt ttgcgaaagt ctgcccaaag cacgtagtgt ttgaagattt      240
189 cggtcctatg caatatgaac ccatgaacca tgtcagggtcc tgacggaagc agcattaagt      300
190 ggatcatcat atgtgccgta gggtagccga gatttagcta acgactttgg ttacgttcgt      360
191 gaattacgtt cgatgcttag gtgcacggtt ttttattttt taaatattaa accgattatt      420
192 aagagttgaa aatatatatt tatttataga agctactttc ttgaagacaa ttcagcgtat      480
193 tatacgtgga acatgtttgt
194      500
195 <210> SEQ ID NO: 6
196 <211> LENGTH: 358
197 <212> TYPE: DNA
198 <213> ORGANISM: Staphylococcus aureus
200 <400> SEQUENCE: 6
201 acttgcaatt aactattaaa atatagtaat atatatcttg ccgtgctagg tggggaggta      60
202 gcggttccct gtactcgaaa tccgctttat gcgaggctta attcctttgt tgaggccgta      120
203 tttttgcgaa gtctgcccaa agcacgtagt gtttgaagat ttcggtccta tgcaatatga      180
204 aacctgaac catgtcaggc cctgacggaa gcagcattaa gtggatcatc atatgtgccg      240
205 tagggtagcc gagatttagc taacgacttt ggttacgttc gtgaattacg ttcgatgctt      300
206 aggtgcacgg ttttttattt tttaaatatt aaaccgatta ttaagagttg aaaatata      358
207
208 <210> SEQ ID NO: 7
209 <211> LENGTH: 276
210 <212> TYPE: DNA
211 <213> ORGANISM: Staphylococcus aureus
213 <400> SEQUENCE: 7
214 cttgccgtgc taggtgggga ggtagcggtt ccctgtactc gaaatccgct ttatgcgagg      60

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215  ctttaattcct ttgttgaggc cgtatttttg cgaagtctgc ccaaagcacg tagtgtttga      120
216  agatttcggg cctatgcaat atgaacccat gaaccatgtc aggtcctgac ggaagcagca      180
217  ttaagtggat catcatatgt gccgtagggt agccgagatt tagctaacga ctttggttac      240
218  gttcgtgaat tacgttcgat gcttaggtgc acggtt      276
220 <210> SEQ ID NO: 8
221 <211> LENGTH: 275
222 <212> TYPE: DNA
223 <213> ORGANISM: Staphylococcus aureus
225 <220> FEATURE:
226 <221> NAME/KEY: misc_feature
227 <222> LOCATION: (1)...(275)
228 <223> OTHER INFORMATION: n = A,T,C or G
230 <400> SEQUENCE: 8
231  aacaatgccg tttcaatata atatttcaaa acatcttgca aatgaattta aatttaccga      60
232  cttctcaaga cgtcgtataa agtaaacaat gatataaatg atttatactt gcaattaact      120
W--> 233  attnaaatat agtaatatat atctttccgt gctagggtggg gaggtagcgg ttccctgtac      180
234  tcgaaatccg ctttatgcga ggcttaattc ctttggtgag gccgtatttt tgcggaagtct      240
235  gcccaaagca cgtagtgttt gaagatttcg gtcct      275

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VERIFICATION SUMMARY

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8